WEST Search History

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DATE: Friday, July 09, 2004

Hide?	Set Name	Query	Hit Count
	DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ		
☐	L1	oligo-dT near$5 primer	0
☐	L2	oligo-dT	3593
☐	L3	L2 near (primer or sequence)	1369
☐	L4	L3 near (detectable marker or label or fluorescen$ or fluorophor$)	2
☐	L5	L3 same (detectable marker or label or fluorescen$ or fluorophor$)	75
☐	L6	L2 same (detectable marker or label or fluorescen$ or fluorophor$)	133
☐	L7	L2 near (tag or marker)	1
☐	L8	L2 same (tag or marker)	147
☐	L9	L3 same (tag or marker)	69
☐	L10	reverse Transcrib$	10356
☐	L11	L10 and (l6 or l7)	72
☐	L12	L10 and (l5 or l8 or l9)	111
☐	L13	(l11 or l12) and (restriction endonuclease or endonuclease or restriction enzyme or sequence-specific cleav$ agent)	100
☐	L14	(ligat$ same adapter same promoter)	937
☐	L15	l13 and l14	8
☐	L16	L15 and amplif$	8
☐	L17	(selective near PCR) or (selective near polymerase chain reaction) or (selective amplification)	3153
☐	L18	(selective near linear amplification)	2
☐	L19	linear amplification	3095
☐	L20	linear PCR	127
☐	L21	differential display	2802
☐	L22	L16 and l17	0
☐	L23	l13 and (adapter same promoter)	9
☐	L24	l13 and (adapter and promoter)	44
☐	L25	(l23 or l24) and (l17 or l19)	18
☐	L26	L25 and l21	0
☐	L27	L24 and l21	3
☐	L28	L13 and l21	22
☐	L29	L28 and (adaptor or adapter)	5

☐	L30	l13 and (adaptor and promoter)	30
☐	L31	l13 and (adaptor same promoter)	5
☐	L32	(ligat$ same adaptor same promoter)	2976
☐	L33	L32 and l13	2
☐	L34	6120996.pn.	2
☐	L35	5695937.pn.	2

END OF SEARCH HISTORY

TERMINAL (ENTER 1, 2, 3, OR ?):2

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* * * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 13:15:31 ON 09 JUL 2004

=> file .biotech caplus
COST IN U.S. DOLLARS SINCE FILE ENTRY TOTAL SESSION
FULL ESTIMATED COST 0.21 0.21

FILES 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT, CAPLUS' ENTERED AT 13:16:11 ON 09 JUL 2004
ALL COPYRIGHTS AND RESTRICTIONS APPLY. SEE HELP USAGETERMS FOR DETAILS.

7 FILES IN THE FILE LIST

=> s kane M?/au or hagel A?/au or dombkowski A?/au
L1 2912 KANE M?/AU OR HAGEL A?/AU OR DOMBKOWSKI A?/AU

=> s l1 and differential display
L2 0 L1 AND DIFFERENTIAL DISPLAY

=> s l1 and express##### gene
L3 0 L1 AND EXPRESS##### GENE

=> s l1 and mRNA
L4 56 L1 AND MRNA

=> s l4 and diffential?
L5 0 L4 AND DIFFENTIAL?

```
=> s l1 and express? mRNA
L6            0 L1 AND EXPRESS? MRNA

=> s differential display or (differentially expressed (5a) mRNA)
L7        20308 DIFFERENTIAL DISPLAY OR (DIFFERENTIALLY EXPRESSED (5A) MRNA)

=> s l1 and l7
L8            0 L1 AND L7

=> d l7 and (oligo-dT (5a) (primer or sequenc?))
'(OLIGO-DT,(5A)' IS NOT VALID HERE

=> s l7 and (oligo-dT (5a) (primer or sequenc?))
L9          128 L7 AND (OLIGO-DT (5A) (PRIMER OR SEQUENC?))

=> s l9 and (detectable marker or marker or tag or label or fluorescen or
fluorophor)
) IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s l9 and reverse transcrib
=>
=>
=>
<------User Break------>

=> s l9 and (reverse transcrib)
) IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=>
=> d his

     (FILE 'HOME' ENTERED AT 13:15:31 ON 09 JUL 2004)

     FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT, CAPLUS'
     ENTERED AT 13:16:11 ON 09 JUL 2004
L1          2912 S KANE M?/AU OR  HAGEL A?/AU OR DOMBKOWSKI A?/AU
L2             0 S L1 AND DIFFERENTIAL DISPLAY
L3             0 S L1 AND EXPRESS##### GENE
L4            56 S L1 AND MRNA
L5             0 S L4 AND DIFFENTIAL?
L6             0 S L1 AND EXPRESS? MRNA
L7         20308 S DIFFERENTIAL DISPLAY OR (DIFFERENTIALLY EXPRESSED (5A) MRNA)
L8             0 S L1 AND L7
L9           128 S L7 AND (OLIGO-DT (5A) (PRIMER OR SEQUENC?))

=> s l9 and (reverse trascrib?)
L10            0 L9 AND (REVERSE TRASCRIB?)

=> s l9 and adaptor
L11            1 L9 AND ADAPTOR

=> d  d his
D NOT VALID FOR HISTORY RANGE
You may enter one of the following:

  1. L1- to display your entire session history
  2. A specific L-number or range of L-numbers to be displayed
  3. L# to display the most recently created L-number
  4. A number, N, to display the N most recent L-numbers
```

ENTER (L1-), L#, OR ?:end

=> l11
L11 IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> d his l11 all
'ALL' IS NOT VALID HERE
For an explanation, enter "HELP DISPLAY HISTORY".

=> d l11 all

L11 ANSWER 1 OF 1 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
AN 95:703492 SCISEARCH
GA The Genuine Article (R) Number: RY760
TI DESCRIPTION OF THE ENTIRE MESSENGER-RNA POPULATION BY A 3'-END CDNA FRAGMENT GENERATED BY CLASS IIS RESTRICTION ENZYMES
AU KATO K (Reprint)
CS JRDC, ERATO, OKAYAMA CELL SWITCHING PROJECT, SAKYO KU, 103-5 TANAKAMONZENCHO, KYOTO 606, JAPAN (Reprint)
CYA JAPAN
SO NUCLEIC ACIDS RESEARCH, (25 SEP 1995) Vol. 23, No. 18, pp. 3685-3690. ISSN: 0305-1048.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 17
AB A novel means of recording the expression status of the total gene population is described, Digestion of cDNA by class IIS restriction enzymes produces a fragment with a poly (A) stretch and a 5' overhang with an unknown sequence, This fragment contains information such as the class IIS enzyme that cuts cDNA nearest to the poly (A) stretch, the sequence of the 5' overhang, and the size of the fragment. Expressed genes can be discriminated and displayed by the fragment as follows: (i) cut the cDNA with one class IIS restriction enzyme; (ii) ligate the digested cDNA to that from a pool of 64 biotinylated adaptors cohesive to all possible overhangs; (iii) digest by other two class IIS enzymes; (iv) recover the ligated molecules with streptavidin-coated paramagnetic beads; (v) perform PCR with the **adaptor-primer** and an anchored **oligo-dT primer**; (vi) separate the amplified fragments by denaturing polyacrylamide gel electrophoresis. Repeat the experiment with 64 adaptors, three enzymes and three anchored oligo-dT primers displays most of the expressed genes, Because redundancy is minimized, this technique is also ideal for generating tags for expressed genes, with which to construct a transcript map of the genome.
CC BIOCHEMISTRY & MOLECULAR BIOLOGY
STP KeyWords Plus (R): **DIFFERENTIAL DISPLAY**; PCR; RNA
RF 93-0362 001; LANGUAGE IMPLEMENTATION; INTEGRATED MEDICAL WORKSTATION; HYPERTEXT SYSTEM; PROGRAMMING ENVIRONMENTS
93-1577 001; DNA RESTRICTION; SITE-SPECIFIC ENDONUCLEASE; COLLECTION OF ANNOTATED PROTEIN SEGMENTS; SBASE DOMAIN LIBRARY; ENZYME DATA-BANK
93-4847 001; HETEROLOGOUS EXPRESSION; CHROMOSOMAL DNA; GENE ENCODING METHYLMALONYL-COENZYME-A MUTASE
RE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)
ADAMS M D	1991	21	1651	SCIENCE
BRENNER S	1989	86	8902	P NATL ACAD SCI USA
DUNBAR B S	1987			2 DIMENSIONAL ELECTR
GUBLER U	1983	25	263	GENE
HORTON R M	1994	16	42	BIOTECHNIQUES
KATO K	1990	2	704	EUR J NEUROSCI

KATO K	1993	6	1	GENOME ANAL GENOME M
KERNIGHAN B W	1984			UNIX PROGRAMMING ENV
KO M S H	1990	18	5705	NUCLEIC ACIDS RES
LIANG P	1993	21	3269	NUCLEIC ACIDS RES
LIANG P	1992	257	967	SCIENCE
SAMBROOK J	1989			MOL CLONING LABORATO
SMITH D R	1992	2	21	PCR METH APPL
SOUTHERN E M	1992	2	412	CURRENT OPINION GENE
SZYBALSKI W	1991	100	13	GENE
UNRAU P	1994	145	163	GENE
WELSH J	1992	20	4965	NUCLEIC ACIDS RES

```
=> d hi
'HI' IS NOT A VALID FORMAT FOR FILE 'SCISEARCH'

The following are valid formats:

The default display format is BIB.

ABS ---- AB
ALL ---- AN, GA, TI, AU, CS, CYA, SO, DT, FS, LA, REC, AB, CC, ST, STP, RF, RE
BIB ---- AN, GA, TI, AU, CS, CYA, SO, DT, FS, LA, REC
CBIB --- CBIB
IABS --- AB
IALL --- AN, GA, TI, AU, CS, CYA, SO, DT, FS, LA, REC, AB, CC, ST, STP, RF, RE
IBIB --- AN, GA, TI, AU, CS, CYA, SO, DT, FS, LA, REC
IND ---- CC, ST, STP, RF
SAM ---- AN, GA, TI, REC, CC, ST, STP, RF
SCAN --- AN, GA, TI, CC, ST, STP, RF (random display without answer numbers)
TRI ---- AN, GA, TI, REC, CC, ST, STP, RF
HIT ---- All fields containing hit terms
KWIC --- All hit terms plus 20 words on either side
OCC ---- List of display fields containing hit terms

Hit terms will be highlighted in all displayable fields except PY.

To display a particular field or fields,  enter the display field
codes.  For a list of display field codes, enter 'HELP DFIELDS'
at an arrow prompt (=>).  Examples of formats include: 'BIB';
'AB'; 'SO,ST'.  You may specify the format fields in any order,
and the information will be displayed in the same order as the
format specification.

The same formats (except for HIT, KWIC, OCC, and SCAN) may be
used with the DISPLAY ACC command to display the record
 for a specified Accession Number.

ENTER DISPLAY FORMAT (BIB):d his
'D' IS NOT A VALID FORMAT FOR FILE 'SCISEARCH'
'HIS' IS NOT A VALID FORMAT FOR FILE 'SCISEARCH'

The following are valid formats:

The default display format is BIB.

ABS ---- AB
ALL ---- AN, GA, TI, AU, CS, CYA, SO, DT, FS, LA, REC, AB, CC, ST, STP, RF, RE
BIB ---- AN, GA, TI, AU, CS, CYA, SO, DT, FS, LA, REC
CBIB --- CBIB
IABS --- AB
IALL --- AN, GA, TI, AU, CS, CYA, SO, DT, FS, LA, REC, AB, CC, ST, STP, RF, RE
IBIB --- AN, GA, TI, AU, CS, CYA, SO, DT, FS, LA, REC
IND ---- CC, ST, STP, RF
SAM ---- AN, GA, TI, REC, CC, ST, STP, RF
```

```
SCAN --- AN, GA, TI, CC, ST, STP, RF (random display without answer numbers)
TRI ---- AN, GA, TI, REC, CC, ST, STP, RF
HIT ---- All fields containing hit terms
KWIC --- All hit terms plus 20 words on either side
OCC ---- List of display fields containing hit terms

Hit terms will be highlighted in all displayable fields except PY.

To display a particular field or fields,  enter the display field
codes.  For a list of display field codes, enter 'HELP DFIELDS'
at an arrow prompt (=>).  Examples of formats include: 'BIB';
'AB'; 'SO,ST'.  You may specify the format fields in any order,
and the information will be displayed in the same order as the
format specification.

The same formats (except for HIT, KWIC, OCC, and SCAN) may be
used with the DISPLAY ACC command to display the record
 for a specified Accession Number.

ENTER DISPLAY FORMAT (BIB):end

=> d his]
'HIS]' IS NOT A VALID FORMAT FOR FILE 'SCISEARCH'

The following are valid formats:

The default display format is BIB.

ABS ---- AB
ALL ---- AN, GA, TI, AU, CS, CYA, SO, DT, FS, LA, REC, AB, CC, ST, STP, RF, RE
BIB ---- AN, GA, TI, AU, CS, CYA, SO, DT, FS, LA, REC
CBIB --- CBIB
IABS --- AB
IALL --- AN, GA, TI, AU, CS, CYA, SO, DT, FS, LA, REC, AB, CC, ST, STP, RF, RE
IBIB --- AN, GA, TI, AU, CS, CYA, SO, DT, FS, LA, REC
IND ---- CC, ST, STP, RF
SAM ---- AN, GA, TI, REC, CC, ST, STP, RF
SCAN --- AN, GA, TI, CC, ST, STP, RF (random display without answer numbers)
TRI ---- AN, GA, TI, REC, CC, ST, STP, RF
HIT ---- All fields containing hit terms
KWIC --- All hit terms plus 20 words on either side
OCC ---- List of display fields containing hit terms

Hit terms will be highlighted in all displayable fields except PY.

To display a particular field or fields,  enter the display field
codes.  For a list of display field codes, enter 'HELP DFIELDS'
at an arrow prompt (=>).  Examples of formats include: 'BIB';
'AB'; 'SO,ST'.  You may specify the format fields in any order,
and the information will be displayed in the same order as the
format specification.

The same formats (except for HIT, KWIC, OCC, and SCAN) may be
used with the DISPLAY ACC command to display the record
 for a specified Accession Number.

ENTER DISPLAY FORMAT (BIB):end

=> f hid
L12       2734 HID

=> d his

     (FILE 'HOME' ENTERED AT 13:15:31 ON 09 JUL 2004)
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```
     FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT, CAPLUS'
     ENTERED AT 13:16:11 ON 09 JUL 2004
L1          2912 S KANE M?/AU OR  HAGEL A?/AU OR DOMBKOWSKI A?/AU
L2             0 S L1 AND DIFFERENTIAL DISPLAY
L3             0 S L1 AND EXPRESS##### GENE
L4            56 S L1 AND MRNA
L5             0 S L4 AND DIFFENTIAL?
L6             0 S L1 AND EXPRESS? MRNA
L7         20308 S DIFFERENTIAL DISPLAY OR (DIFFERENTIALLY EXPRESSED (5A) MRNA)
L8             0 S L1 AND L7
L9           128 S L7 AND (OLIGO-DT (5A) (PRIMER OR SEQUENC?))
L10            0 S L9 AND (REVERSE TRASCRIB?)
L11            1 S L9 AND ADAPTOR
L12         2734 F HID

=> l9 and (restriction enzyme or restriction endonuclease or endonuclease)
L9 IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s l9 and (restriction enzyme or restriction endonuclease or endonuclease)
L13            9 L9 AND (RESTRICTION ENZYME OR RESTRICTION ENDONUCLEASE OR ENDON
                 UCLEASE)

=> dup rem l9
PROCESSING COMPLETED FOR L9
L14           58 DUP REM L9 (70 DUPLICATES REMOVED)

=> dum rel l13
DUM IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> dup renm l13
ENTER REMOVE, IDENTIFY, ONLY, OR (?):l13
'L104' IS NOT VALID HERE
Enter "REMOVE" to identify and remove duplicate answers.
Enter "IDENTIFY" to identify duplicate answers in the answer set.
Enter "ONLY" to identify and create an answer set containing only
duplicate records.
ENTER REMOVE, IDENTIFY, ONLY, OR (?):end

=> dup rem l13
PROCESSING COMPLETED FOR L13
L15            5 DUP REM L13 (4 DUPLICATES REMOVED)

=> d ibib abs l15 1-5

L15   ANSWER 1 OF 5  BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
ACCESSION NUMBER: 2004-02692  BIOTECHDS
TITLE:            New annealing control primer capable of improving primer
                  annealing specificity in association with the alteration of
                  primer annealing temperature, useful for selectively
                  amplifying a target nucleic acid sequence;
                     DNA primer for mRNA differential expression detection
AUTHOR:           CHUN J Y
PATENT ASSIGNEE:  SEEGENE INC
PATENT INFO:      WO 2003093509 13 Nov 2003
APPLICATION INFO: WO 2002-KR816 1 May 2002
PRIORITY INFO:    WO 2002-816 1 May 2002; WO 2002-816 1 May 2002
DOCUMENT TYPE:    Patent
LANGUAGE:         English
OTHER SOURCE:     WPI: 2004-022665 [02]
```

AN 2004-02692 BIOTECHDS

AB DERWENT ABSTRACT:

NOVELTY - Annealing control primer capable of improving primer annealing specificity in association with the alteration of primer annealing temperature comprises a 3' and 5'-end portions separated by at least 2 deoxyinosine residues, universal bases or non-discriminatory base analogs, is new.

DETAILED DESCRIPTION - Annealing control primer capable of improving primer annealing specificity in association with the alteration of primer annealing temperature comprises a 3' and 5'-end portions separated by at least 2 deoxyinosine residues, universal bases or non-discriminatory base analogs, where the presence of deoxyinosine group positioned between the 3' and 5'-end portions plays as a switch in controlling primer annealing to a template nucleic acid in association with annealing temperature during PCR in order to interrupt the annealing of the 5'-end portion and limit primer annealing to the 3'-end portion at a first annealing temperature. The 5'-end portion comprises a universal primer sequence and serves as a universal priming site for subsequent amplification of reaction product generated from the annealing and extension of the 3'-end portion sequence to the template nucleic acid with the annealing of the 3'-end portion bothered or interrupted at a second annealing temperature. INDEPENDENT CLAIMS are also included for the following: (1) a kit comprising the annealing control primer; (2) selectively amplifying a target nucleic acid sequence from a nucleic acid molecule or mixture of nucleic acids using annealing control primers; (3) detecting DNA complementary to **differentially expressed mRNA** in two or more nucleic acid samples using annealing control primers; (4) amplifying a target cDNA fragment comprising 5'-end region corresponding to the 5'-end of mRNA using annealing control primers; (5) amplifying a population of full-length double-stranded cDNAs complementary to mRNAs using annealing control primers; where the cDNAs comprise the complete 5'-end sequence information of the mRNAs; and (6) amplifying 5'-enriched double-stranded cDNA molecules complementary to mRNA molecules using annealing control primers.

BIOTECHNOLOGY - Preferred Primer: The annealing control primer has the general formula 5'-dNx-dIy-dNz-3. dNx = represents the 5'-end portion and contains a preselected arbitrary nucleotide sequence; dNz = represents the 3'-end portion; dIy = represents a deoxyinosine group having at least 2 deoxyinosine residues; dN = represents a deoxyribonucleotide; x, y or z = independently represents an integer; x = is the number of nucleotides in the 5'-end portion (which is an integer of 15-60); y = is the number of deoxyinosine residues separating the 3' and 5'-end portions (which is at least 3 or an integer of 2-15); and z = is the number of nucleotides in the 3'-end portion (which is an integer of 6-30). The deoxyribonucleotides comprise dAMP, dTMP, cDMP, dGMP, modified nucleotides or non-natural nucleotides. DNx includes a sequence that is recognized by a **restriction endonuclease.** It comprises at least one nucleotide with a hapten group. DNz is complementary to a target sequence in the template nucleic acid or to a consensus sequence found in a gene family. It is a degenerate sequence comprising combinations of nucleotides encoding a predetermined amino acid sequence. It comprises at least one ribonucleotide. It is a random nucleotide sequence. It is a deoxythymidine nucleotide sequence. It comprises at least 10 contiguous deoxythymidine nucleotides having 3'-NV, where V is deoxyadenosine, deoxycytidine or deoxyguanosine, and N is deoxythymidine, deoxyadenosine, deoxycytidine or deoxyguanosine The template nucleic acid of the annealing control primer is mRNA or cDNA derived from mRNA, or is single or double stranded DNA. The first annealing temperature of the annealing control primer should be lower than the second annealing temperature or is 37-65 or 50-72 degreesC. Preferred Method: Selectively amplifying a target nucleic acid sequence from a nucleic acid molecule or mixture of nucleic acids using annealing control primers comprises carrying out a two-stage PCR comprising: (1) amplifying the target nucleic acid sequence in a first-stage PCR comprising at least two cycles of primer annealing,

primer extending and denaturing, by annealing a pair of annealing control primers to the target nucleic acid sequence at a first annealing temperature under conditions sufficient for template driven enzymatic DNA synthesis to occur; extending the primers to obtain first amplification product; denaturing the first amplification product to obtain denatured amplification product; and (2) re-amplifying the denatured amplification product at the second annealing temperature, which is high stringent conditions, in a second-stage PCR comprising at least one cycle of annealing, primer extending and denaturing, by annealing universal primers corresponding to the 5'-end portion sequences of the annealing control primers to the 5'-end sequences of the denatured amplification product generated by the annealing control primers from step (1) and extending the primers to generate second amplification product. The target nucleic acid sequence is DNA or RNA. The first-stage PCR is repeated at least twice. The second-stage PCR is repeated at least 10 times. The first annealing temperature is at least 40 degreesC, while the second annealing temperature is at least 50 degreesC. Detecting DNA complementary to **differentially expressed mRNA** in two or more nucleic acid samples using annealing control primers comprises: (1) providing a first sample of nucleic acids representing a first population of mRNA transcripts and a second sample of nucleic acids representing a second population of mRNA transcripts; (2) separately contacting each of the first and second nucleic acid samples with a first annealing control primer; (3) reverse transcribing the **differentially expressed mRNA** to which the first annealing control primer hybridizes to produce a first population of DNA strands that are complementary to the **differentially expressed mRNA** in the first nucleic acid sample to which the first annealing control primer hybridizes, and a second population of DNA strands that are complementary to the **differentially expressed mRNA** in the second nucleic acid sample to which the first annealing control primer hybridizes; (4) purifying and quantifying each of the first and second populations of complementary DNA strands; (5) contacting each of the first and second populations of complementary DNA strands with a second annealing control primer at a first annealing temperature, where the second annealing control primer has a hybridizing sequence sufficiently complementary to the first and second populations of DNA strands; (6) extending the second annealing control primer using DNA polymerase to produce a second DNA strand complementary to the first and second populations of DNA strands; (7) amplifying each second DNA strand obtained from step (6) at a second annealing temperature, by at least one PCR cycle to obtain the first and second populations of amplification products using 2 universal primers; and (8) comparing the presence or level of individual amplification products in the first and second populations of amplification products. The method further comprises isolating the amplified cDNA product and cloning the isolated cDNA product into a vector. The comparison comprises resolving each of the first and second populations of amplification products by gel electrophoresis through an ethidium bromide-stained agarose gel and comparing the presence or level of bands of a particular size. The nucleotide sequence of each of the first and second annealing control primers comprises at least one nucleotide with a hapten group. The universal primers comprise a sequence having 21-22 bp. The first nucleic acid sample comprises mRNA expressed in a first cell and the second nucleic acid sample comprises mRNA expressed in a second cell. The first nucleic acid sample comprises mRNA expressed in a tumorigenic cell and the second nucleic acid sample comprises mRNA expressed in a normal cell. The first annealing control primer has the general formula of 5'-dN15-30-dI2-10-dT10-20-3'. dN = represents a deoxyribonucleotide and contains preselected arbitrary nucleotide sequence; dI = represents a deoxyinosine, universal base or non-discriminatory base analog; is 1-(2'-deoxy-beta-D-ribofuranosyl)-3-nitropyrole or 5-Nitroindole; dT = represents a deoxythymidine; further comprises 3'-V. The first annealing control primer comprises a sequence having comprises a sequence having 37

bp. The second annealing control primer has the general formula of 5'-dN15-30-dI2-10-dN8-15-3', where the formula follows the same rule of the formula 5'-dNx-dIy-dNz-3. It comprises a sequence having 32-40 bp. Amplifying a target cDNA fragment comprising 5'-end region corresponding to the 5'-end of mRNA using annealing control primers comprises: (1) contacting the mRNA with a conventional **Oligo dT primer** or random **primer** as a cDNA synthesis primer under conditions sufficient for template driven enzymatic DNA synthesis to occur; (2) reverse transcribing the mRNA to which cDNA synthesis primer hybridizes to produce first-strand cDNA that is complementary to the mRNA to which the cDNA synthesis primer hybridizes, resulting in forming mRNA-cDNA intermediate; (3) permitting cytosine residues to be tailed at the 3'-end of the first strand cDNA by the terminal transferase reaction of reverse transcriptase in the presence of manganese under the form of the mRNA-cDNA intermediate; (4) contacting a first annealing control primer to the cytosine tail at the 3'-end of the first cDNA strand in the form of the mRNA-cDNA intermediate; where the first annealing control primer comprises at least 3 guanine residues at its 3'-end to hybridize the cytosine tail of the 3'-end of the first cDNA strand; (5) extending the tailed 3'-end of the first strand cDNA to generate an additional sequence complementary to the first annealing control primer using reverse transcriptase; where the first annealing control primer is used as a template in the extension reaction; (6) synthesizing the second-strand cDNA of the extended first-strand cDNA using a universal primer by at least one cycle of PCR; where the universal primer has a sequence complementary to the 5'-end extended sequence of the first-strand cDNA; (7) synthesizing a target cDNA strand using a second annealing control primer at a first annealing temperature by at least one PCR cycle; and (8) amplifying the target cDNA strand using 2 universal primers at a second annealing temperature, which is high stringent conditions, by at least one PCR cycle; where the universal primers have sequences complementary to both 3'- and 5'-ends of the target cDNA strand, which comprises the sequences of the first and second annealing control primers at both 3'- and 5'-ends. Amplifying a population of full-length double-stranded cDNAs complementary to mRNAs using annealing control primers; where the cDNAs comprise the complete 5'-end sequence information of the mRNAs comprises: (1) contacting the mRNAs with a first annealing control primer under conditions sufficient for template driven enzymatic DNA synthesis to occur, where the first annealing control primer comprises a hybridizing sequence at 3'-end portion complementary to the polyA tail of the mRNAs to hybridize; (2) reverse transcribing the mRNAs to which the first annealing control primer hybridizes to produce first strand cDNA sequences that are complementary to the mRNAs to which the first annealing control primer hybridizes, resulting in forming mRNA-cDNA intermediates; (3) permitting cytosine residues to be tailed at the 3'-end of the first strand cDNAs by the terminal transferase reaction of reverse transcriptase in the presence of manganese under the form of the mRNA-cDNA intermediates; (4) contacting a second annealing control primer to the cytosine tails at the 3'-end of the first cDNA strands in the form of the mRNA-cDNA intermediates, where the second annealing control primer comprises at least 3 guanine residues at its 3'-end to hybridize the cytosine tails of the 3'-end of the first cDNA strands; (5) extending the tailed 3'-ends of the first strand cDNAs to generate additional sequences complementary to the second annealing control primer using reverse transcriptase, where the second annealing control primer is used as a template in the extension reaction; and (6) amplifying the extended first strand cDNAs using 2 universal primers to obtain amplification products of full-length cDNAs complementary to the mRNAs, by at least one cycle of PCR. The method further comprises introducing the double-stranded cDNA molecules obtained from step (6) into vectors. Amplifying 5'-enriched double-stranded cDNA molecules complementary to mRNA molecules using annealing control primers comprises: (1) contacting the mRNA molecules with a first annealing control primer under conditions sufficient for template driven enzymatic DNA synthesis to occur; where the first

annealing control primer comprises at least 6 random nucleotide sequences at 3'-end portion; and (2) performing steps (2)-(6) to amplify 5'-enriched double-stranded cDNA molecules.

USE - The annealing control primer is useful for selectively amplifying a target nucleic acid sequence from a nucleic acid molecule or mixture of nucleic acids, for detecting DNA complementary to **differentially expressed mRNA** in two or more nucleic acid samples or for amplifying a population of full-length double-stranded cDNAs complementary to mRNAs using annealing control primers.

ADVANTAGE - Primer annealing specificity is improved by the effect of the deoxyinosine residue group on the annealing of 3'- and 5'-end portions of ACP in accordance with the alteration of annealing temperature, which requires two stage PCR amplifications. Amplification of non-specific PCR products is interrupted by two-stage PCR amplifications, which are performed at low and high stringent conditions. Mispriming which is a major cause of false product amplification during PCR can be significantly minimized. The efficiency of PCR amplification is increased, which makes it easier to detect rare mRNAs. The reproducibility of PCR products is increased, which saves a great amount of time and cost. Agarose gel electrophoresis followed by ethidium bromide staining can be used for detecting differentially displayed RT-PCR products. The background problems arising from contamination of the primers used for cDNA synthesis for 5'- or 3'-rapid amplification of cDNA ends can be eliminated.

EXAMPLE - No relevant examples given. (136 pages)

L15 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1999:538415 CAPLUS
DOCUMENT NUMBER: 132:742
TITLE: A Novel Strategy for Identifying Differential Gene Expression: An Improved Method of **Differential Display** Analysis
AUTHOR(S): Kohroki, Junya; Tsuchiya, Mikako; Fujita, Sayaka; Nakanishi, Tsuyoshi; Itoh, Norio; Tanaka, Keiichi
CORPORATE SOURCE: Department of Toxicology, Graduate School of Pharmaceutical Sciences, Osaka University, Suita, Osaka, 565-0871, Japan
SOURCE: Biochemical and Biophysical Research Communications (1999), 262(2), 365-367
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB We propose a novel alternative approach, an advanced method for recently developed strategies, for identifying differentially expressed genes. Firstly, double-stranded cDNAs were digested using Sau3AI and the 3'-end restriction fragments of the cDNA were ligated to a double-stranded adapter. Next, the restriction fragments were directly amplified using several combinations of adapter-specific primers and FITC-labeled oligo dT primers. The selected cDNA fragments were displayed on a polyacrylamide gel. Neither nested PCR nor purification of 3'-end fragments are necessary. We examined the validity of this approach by evaluating gene expression changes during granulocytic differentiation of HL-60 cells. This method can theor. detect almost all gene expression changes more rapidly and through simpler manipulations than by any other approach. (c) 1999 Academic Press.

REFERENCE COUNT: 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L15 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1999:704522 CAPLUS
DOCUMENT NUMBER: 132:132862
TITLE: A Novel Strategy for Identifying Differential Gene Expression: An Improved Method of **Differential**

Display Analysis. [Erratum to document cited in CA132:742]
AUTHOR(S): Kohroki, Junya; Tsuchiya, Mikako; Fujita, Sayaka; Nakanishi, Tsuyoshi; Itoh, Norio; Tanaka, Keiichi
CORPORATE SOURCE: Dep. Toxicology, Graduate School Pharmaceutical Sciences, Osaka Univ., Suita, Osaka, 565-0871, Japan
SOURCE: Biochemical and Biophysical Research Communications (1999), 265(1), 272
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB On page 365, column 2, line 18, and on page 366, column 2, line 13 to page 367, column 1, line 1, the sequence of the adapter primer was incorrect as printed. The sequence should read "(5'-GTCGACATGAGTGTGATCN1N2-3',..." instead of "(5'-GTCGACATGAGTGTGAN1N2-3',..." and "5'-GTCGACATGAGTGTGANN-3'...", resp., as printed. (c) 1999 Academic Press.

L15 ANSWER 4 OF 5 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2000064167 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10596370
TITLE: The coupling of **differential display** and AFLP approaches for nonradioactive mRNA fingerprinting.
AUTHOR: Ivashuta S; Imai R; Uchiyama K; Gau M
CORPORATE SOURCE: Hokkaido National Agricultural Experiment Station, Sapporo, Japan.. sergey@cryo.affrc.go.jp
SOURCE: Molecular biotechnology, (1999 Sep) 12 (2) 137-41.
Journal code: 9423533. ISSN: 1073-6085.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199912
ENTRY DATE: Entered STN: 20000114
Last Updated on STN: 20000114
Entered Medline: 19991230
AB We have modified the **differential display** of 3'-end restriction fragments of cDNA technique by combining it with the amplified fragment length polymorphism (AFLP) approach and silver staining. Modified oligo-dT primers were used for a reverse transcription step. ds cDNA was digested with the Mse I **restriction enzyme** and then ligated with an AFLP adapter. The modified template was amplified with oligo-dT primers in a preamplification step (asymmetric PCR) that enriched the template for 3'-end sequences; subsequently, the enriched template was amplified with an AFLP primer having a selective extension and an anchored **oligo-dT primer** (conventional PCR step). We demonstrated that the asymmetric preamplification step facilitates the preferential amplification of 3'-end fragments and the resulting PCR products can be clear resolved on silver-stained gel. The presented procedure takes advantages of silver-stained gels, generates reproducible display patterns, and allows reliable reamplification of isolated fragments which contain both upstream and downstream primer sequences.

L15 ANSWER 5 OF 5 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
ACCESSION NUMBER: 95:703492 SCISEARCH
THE GENUINE ARTICLE: RY760
TITLE: DESCRIPTION OF THE ENTIRE MESSENGER-RNA POPULATION BY A 3'-END CDNA FRAGMENT GENERATED BY CLASS IIS RESTRICTION ENZYMES
AUTHOR: KATO K (Reprint)
CORPORATE SOURCE: JRDC, ERATO, OKAYAMA CELL SWITCHING PROJECT, SAKYO KU, 103-5 TANAKAMONZENCHO, KYOTO 606, JAPAN (Reprint)
COUNTRY OF AUTHOR: JAPAN
SOURCE: NUCLEIC ACIDS RESEARCH, (25 SEP 1995) Vol. 23, No. 18, pp.

3685-3690.
ISSN: 0305-1048.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 17
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB A novel means of recording the expression status of the total gene population is described, Digestion of cDNA by class IIS restriction enzymes produces a fragment with a poly (A) stretch and a 5' overhang with an unknown sequence, This fragment contains information such as the class IIS enzyme that cuts cDNA nearest to the poly (A) stretch, the sequence of the 5' overhang, and the size of the fragment. Expressed genes can be discriminated and displayed by the fragment as follows: (i) cut the cDNA with one class IIS **restriction enzyme**; (ii) ligate the digested cDNA to that from a pool of 64 biotinylated adaptors cohesive to all possible overhangs; (iii) digest by other two class IIS enzymes; (iv) recover the ligated molecules with streptavidin-coated paramagnetic beads; (v) perform PCR with the adaptor-**primer** and an anchored **oligo-dT primer**; (vi) separate the amplified fragments by denaturing polyacrylamide gel electrophoresis. Repeat the experiment with 64 adaptors, three enzymes and three anchored oligo-dT primers displays most of the expressed genes, Because redundancy is minimized, this technique is also ideal for generating tags for expressed genes, with which to construct a transcript map of the genome.

=> d his

(FILE 'HOME' ENTERED AT 13:15:31 ON 09 JUL 2004)

FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT, CAPLUS' ENTERED AT 13:16:11 ON 09 JUL 2004

```
L1          2912 S KANE M?/AU OR  HAGEL A?/AU OR DOMBKOWSKI A?/AU
L2             0 S L1 AND DIFFERENTIAL DISPLAY
L3             0 S L1 AND EXPRESS##### GENE
L4            56 S L1 AND MRNA
L5             0 S L4 AND DIFFENTIAL?
L6             0 S L1 AND EXPRESS? MRNA
L7         20308 S DIFFERENTIAL DISPLAY OR (DIFFERENTIALLY EXPRESSED (5A) MRNA)
L8             0 S L1 AND L7
L9           128 S L7 AND (OLIGO-DT (5A) (PRIMER OR SEQUENC?))
L10            0 S L9 AND (REVERSE TRASCRIB?)
L11            1 S L9 AND ADAPTOR
L12         2734 F HID
L13            9 S L9 AND (RESTRICTION ENZYME OR RESTRICTION ENDONUCLEASE OR EN
L14           58 DUP REM L9 (70 DUPLICATES REMOVED)
L15            5 DUP REM L13 (4 DUPLICATES REMOVED)
```

=> s l9 and (linear amplification or selective amplification)

```
L16            5 L9 AND (LINEAR AMPLIFICATION OR SELECTIVE AMPLIFICATION)
```

=> d ibib abs l16 1-5

L16 ANSWER 1 OF 5 MEDLINE on STN
ACCESSION NUMBER: 96216735 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8645264
TITLE: Combining the technique of RNA fingerprinting and **differential display** to obtain **differentially expressed mRNA.**
AUTHOR: Diachenko L B; Ledesma J; Chenchik A A; Siebert P D
CORPORATE SOURCE: CLONTECH Laboratories, Inc., Palo Alto, California 94303-4230, USA.
SOURCE: Biochemical and biophysical research communications, (1996 Feb 27) 219 (3) 824-8.

Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199607
ENTRY DATE: Entered STN: 19960726
Last Updated on STN: 19960726
Entered Medline: 19960715

AB We have modified recently developed methods of RNA fingerprinting and **differential display** based on arbitrarily primed PCR which can be used for detection and cloning of differentially expressed mRNAs. Our protocol requires only a single cDNA synthesis for each different RNA sample, in contrast to the multiple cDNA reactions required for **differential display** method, followed by **selective amplification** of cDNA **sequence** fraction by arbitrary and **oligo(dT)** primers. We have shown that the longer primers (25-29-mers) allow the use of optimal dNTP concentration and higher stringency PCR. Further improvements include using TaqStart antibody for hot start PCR and thermostable enzyme mixes suitable for long-distance PCR. Long-distance PCR enables the method to display bands of up to 2 kb and should result in a higher fidelity of PCR products to the original RNA template. When these improvements are combined the resulting method is highly reproducible, and more than 85% of the differentially expressed bands can be confirmed by Northern blot analysis.

L16 ANSWER 2 OF 5 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 96111972 EMBASE
DOCUMENT NUMBER: 1996111972
TITLE: Combining the technique of RNA fingerprinting and **differential display** to obtain **differentially expressed mRNA.**
AUTHOR: Diachenko L.B.; Ledesma J.; Chenchik A.A.; Siebert P.D.
CORPORATE SOURCE: CLONTECH Laboratories Inc, 1020 East Meadow Circle,Palo Alto, CA 94303-4230, United States
SOURCE: Biochemical and Biophysical Research Communications, (1996) 219/3 (824-828).
ISSN: 0006-291X CODEN: BBRCA
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

AB We have modified recently developed methods of RNA fingerprinting and **differential display** based on arbitrarily primed PCR which can be used for detection and cloning of differentially expressed mRNAs. Our protocol requires only a single cDNA synthesis for each different RNA sample, in contrast to the multiple cDNA reactions required for **differential display** method, followed by **selective amplification** of cDNA **sequence** fraction by arbitrary and **oligo(dT)** primers. We have shown that the longer primers (25-29-mers) allow the use of optimal dNTP concentration and higher stringency PCR. Further improvements include using TaqStart antibody for hot start PCR and thermostable enzyme mixes suitable for long-distance PCR. Long-distance PCR enables the method to display bands of up to 2 kb and should result in a higher fidelity of PCR products to the original RNA template. When these improvements are combined the resulting method is highly reproducible, and more than 85% of the differentially expressed bands can be confirmed by Northern blot analysis.

L16 ANSWER 3 OF 5 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: 1996:219632 BIOSIS
DOCUMENT NUMBER: PREV199698775761
TITLE: Combining the technique of RNA fingerprinting and **differential display** to obtain **differentially expressed mRNA.**
AUTHOR(S): Diachenko, Luda B.; Ledesma, John; Chenchik, Alex A.; Siebert, Paul D.
CORPORATE SOURCE: CLONTECH Lab. Inc., 1020 East Meadow Circle, Palo Alto, CA 94303-4230, USA
SOURCE: Biochemical and Biophysical Research Communications, (1996) Vol. 219, No. 3, pp. 824-828.
CODEN: BBRCA9. ISSN: 0006-291X.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 8 May 1996
Last Updated on STN: 8 May 1996

AB We have modified recently developed methods of RNA fingerprinting and **differential display** based on arbitrarily primed PCR which can be used for detection and cloning of differentially expressed mRNAs. Our protocol requires only a single cDNA synthesis for each different RNA sample, in contrast to the multiple cDNA reactions required for **differential display** method, followed by **selective amplification** of cDNA **sequence** fraction by arbitrary and **oligo(dT)** primers. We have shown that the longer primers (25-29-mers) allow the use of optimal dNTP concentration and higher stringency PCR. Further improvements include using TaqStart antibody for hot start PCR and thermostable enzyme mixes suitable for long-distance PCR. Long-distance PCR enables the method to display bands of up to 2 kb and should result in a higher fidelity of PCR products to the original RNA template. When these improvements are combined the resulting method is highly reproducible, and more than 85% of the differentially expressed bands can be confirmed by Northern blot analysis.

L16 ANSWER 4 OF 5 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
ACCESSION NUMBER: 96:211116 SCISEARCH
THE GENUINE ARTICLE: TZ799
TITLE: COMBINING THE TECHNIQUE OF RNA FINGERPRINTING AND **DIFFERENTIAL DISPLAY** TO OBTAIN DIFFERENTIALLY EXPRESSED MESSENGER-RNA
AUTHOR: DIACHENKO L B (Reprint); LEDESMA J; CHENCHIK A A; SIEBERT P D
CORPORATE SOURCE: CLONTECH LABS INC, 1020 E MEADOW CIRCLE, PALO ALTO, CA, 94303 (Reprint)
COUNTRY OF AUTHOR: USA
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (27 FEB 1996) Vol. 219, No. 3, pp. 824-828.
ISSN: 0006-291X.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 12
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB We have modified recently developed methods of RNA fingerprinting and **differential display** based on arbitrarily primed PCR which can be used for detection and cloning of differentially expressed mRNAs. Our protocol requires only a single cDNA synthesis for each different RNA sample, in contrast to the multiple cDNA reactions required for **differential display** method, followed by **selective amplification** of cDNA **sequence** fraction by arbitrary and **oligo(dT)** primers. We have shown that the longer primers (25-29-mers) allow the use of optimal dNTP concentration and higher stringency PCR. Further improvements include using TaqSart antibody for hot start PCR and thermostable enzyme mixes suitable for long-distance PCR. Long-distance PCR enables the method to

display bands of up to 2 kb and should result in a higher fidelity of PCR products to the original RNA template. When these improvements are combined the resulting method is highly reproducible, and more than 85% of the differentially expressed bands can be confirmed by Northern blot analysis. (C) 1996 Academic Press, Inc.

L16 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1996:162465 CAPLUS
DOCUMENT NUMBER: 125:106264
TITLE: Combining the technique of RNA fingerprinting and **differential display** to obtain **differentially expressed mRNA**
AUTHOR(S): Diachenko, Luda B.; Ledesma, John; Chenchik, Alex A.; Siebert, Paul D.
CORPORATE SOURCE: CLONTECH Laboratories, Inc., Palo Alto, CA, 94303-4230, USA
SOURCE: Biochemical and Biophysical Research Communications (1996), 219(3), 824-28
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Academic
DOCUMENT TYPE: Journal
LANGUAGE: English
AB We have modified recently developed methods of RNA fingerprinting and **differential display** based on arbitrarily primed PCR which can be used for detection and cloning of differentially expressed mRNAs. Our protocol requires only a single cDNA synthesis for each different RNA sample, in contrast to the multiple cDNA reactions required for **differential display** method, followed by **selective amplification** of cDNA **sequence** fraction by arbitrary and **oligo(dT)** primers. We have shown that the longer primers (25-29-mers) allow the use of optimal dNTP concentration and higher stringency PCR. Further improvements include using TaqStart antibody for hot start PCR and thermostable enzyme mixes suitable for long-distance PCR. Long-distance PCR enables the method to display bands of up to 2 kb and should result in a higher fidelity of PCR products to the original RNA template. When these improvements are combined the resulting method is highly reproducible, and more than 85% of the differentially expressed bands can be confirmed by Northern blot anal.

=> d his

(FILE 'HOME' ENTERED AT 13:15:31 ON 09 JUL 2004)

FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT, CAPLUS' ENTERED AT 13:16:11 ON 09 JUL 2004

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L1          2912 S KANE M?/AU OR  HAGEL A?/AU OR DOMBKOWSKI A?/AU
L2             0 S L1 AND DIFFERENTIAL DISPLAY
L3             0 S L1 AND EXPRESS##### GENE
L4            56 S L1 AND MRNA
L5             0 S L4 AND DIFFENTIAL?
L6             0 S L1 AND EXPRESS? MRNA
L7         20308 S DIFFERENTIAL DISPLAY OR (DIFFERENTIALLY EXPRESSED (5A) MRNA)
L8             0 S L1 AND L7
L9           128 S L7 AND (OLIGO-DT (5A) (PRIMER OR SEQUENC?))
L10            0 S L9 AND (REVERSE TRASCRIB?)
L11            1 S L9 AND ADAPTOR
L12         2734 F HID
L13            9 S L9 AND (RESTRICTION ENZYME OR RESTRICTION ENDONUCLEASE OR EN
L14           58 DUP REM L9 (70 DUPLICATES REMOVED)
L15            5 DUP REM L13 (4 DUPLICATES REMOVED)
L16            5 S L9 AND (LINEAR AMPLIFICATION OR SELECTIVE AMPLIFICATION)
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=> s liang ?/au

L17 73006 LIANG ?/AU

=> s l17 and differential display
L18 271 L17 AND DIFFERENTIAL DISPLAY

=> s l18 and oligo dT
L19 27 L18 AND OLIGO DT

=> s l19 and (restriction endonuclease or restriction enzyme or endonuclease)
L20 1 L19 AND (RESTRICTION ENDONUCLEASE OR RESTRICTION ENZYME OR ENDONUCLEASE)

=> d all

L20 ANSWER 1 OF 1 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
AN 95033514 EMBASE
DN 1995033514
TI **Differential display** using one-base anchored **oligo-dT** primers.
AU **Liang P.**; Zhu W.; Zhang X.; Guo Z.; O'Connell R.P.; Averboukh L.; Wang F.; Pardee A.B.
CS Division Cell Growth and Regulation, Dana-Farber Cancer Institute,Boston, MA 02115, United States
SO Nucleic Acids Research, (1994) 22/25 (5763-5764).
ISSN: 0305-1048 CODEN: NARHAD
CY United Kingdom
DT Journal; Article
FS 022 Human Genetics
029 Clinical Biochemistry
LA English
CT Medical Descriptors:
*gene expression
animal cell
article
cell transformation
controlled study
dna sequence
fibroblast
gene amplification
molecular cloning
nonhuman
northern blotting
polymerase chain reaction
priority journal
rat
rna analysis
Drug Descriptors:
*oligonucleotide
messenger rna
polyadenylic acid
primer rna
restriction endonuclease
RN (polyadenylic acid) 24937-83-5

=> end
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